

70681
STIC-Biotech/ChemLib

184292
From: Myers, Carla
Sent: Wednesday, April 05, 2006 11:26 AM
To: STIC-Biotech/ChemLib
Subject: sequence search for 09/701,132

Please search:

a) an n-mer search for fragments of 10 or more nucleotides of SEQ ID NO: 13.
(i.e., the claims are limited to nucleic acids consisting of 10 or more nucleotides of SEQ ID NO: 13, so I would like to find references that include only the sequences of SEQ ID NO: 13)

b) nucleotides 586 to 810 of SEQ ID NO: 13.

c) SEQ ID NO: 57

d) nucleotides 79 to 6471 of SEQ ID NO: 56

e) nucleotides 13261 to 13821 of SEQ ID NO: 56

Please provide a printout of the first 40 results.

Thank you

Carla Myers
AU 1634
Remsen Bldg / Rm 2E79
Mailbox: REM 2C70
571-272-0747

RECEIVED
APR - 5 2006
STIC-BIOTECH DIVISION
(STIC)

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

WEST Search History

[Hide Items](#)[Restore](#)[Clear](#)[Cancel](#)

DATE: Tuesday, June 06, 2006

Hide?	Set Name	Query	Hit Count
<i>DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=ADJ</i>			
<input type="checkbox"/>	L9	coli same (O adj serotype)	15
<input type="checkbox"/>	L8	L7 and (pcr or primer or probe or amplifi\$ or hybridi\$)	342
<input type="checkbox"/>	L7	(flagella or flagellin) same coli	391
<input type="checkbox"/>	L6	L3 and (H or O)	337
<input type="checkbox"/>	L5	L2 and ((H adj serotype) or (O adj serotype))	6
<input type="checkbox"/>	L4	L3 and ((H adj serotype) or (O adj serotype))	4
<input type="checkbox"/>	L3	L2 and (pcr or primers or hybridi\$ or probe)	354
<input type="checkbox"/>	L2	L1 same coli	405
<input type="checkbox"/>	L1	flagellin or flmA or flkA or flic or fliC or flagella	2513

END OF SEARCH HISTORY

gi|290160|gb|L15643.1|DOGP23602 Dog (Clone: CXX.236) primer for STS 236, 3' end
Length=22

Score = 28.2 bits (14), Expect = 1.0
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

```
Query  1047  TGGTAACAATAAAG  1060
          |||||
Sbjct  15    TGGTAACAATAAAG  2
```

> gi|29565480|emb|AJ544052.1|DME544052 Drosophila melanogaster partial snmRNA gene for :
RNA, clone Dm-173
Length=31

Score = 26.3 bits (13), Expect = 4.0
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

```
Query  471  CGATGGCGCGCAG  483
          |||||
Sbjct  19    CGATGGCGCGCAG  31
```

> gi|3135150|dbj|D88711.1| Hepatitis G virus RNA for polyprotein (N3 region), partial cc
isolate D77
Length=43

Score = 26.3 bits (13), Expect = 4.0
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query  357  CCTTGCTGAAAAT  369
          |||||
Sbjct  28    CCTTGCTGAAAAT  16
```

> gi|51947926|gb|AY733678.1| Macaca mulatta isolate 96E025-MDS1 MLV-derived vector prov:
integration site
Length=50

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

```
Query  1133  CTACCACCAACC  1144
          |||||
Sbjct  15    CTACCACCAACC  26
```

> gi|255419|gb|S44672.1|S44670S2 snRNA U2-1 [Tetrahymena thermophila, Genomic, 50 nt, se
2 of 2]
Length=50

Score = 24.3 bits (12), Expect = 16
Identities = 15/16 (93%), Gaps = 0/16 (0%)
Strand=Plus/Plus

```
Query 845 ACAAAAAAGCTTCTTT 860
          |||||
Sbjct 24 ACAAAAAACCTTCTTT 39
```

> [gi|62816380|emb|AJ965727.1|](#) Pisum sativum PDR1 retrotransposon partial right terminal clone 1006-R11
Length=48

Score = 24.3 bits (12), Expect = 16
Identities = 15/16 (93%), Gaps = 0/16 (0%)
Strand=Plus/Minus

```
Query 416 CTATCAATCTGGCAAA 431
          |||||
Sbjct 33 CTATCAATCTGACAAA 18
```

Score = 22.3 bits (11), Expect = 62
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Minus

```
Query 1256 ACAACCTGTCT 1266
          |||||
Sbjct 45 ACAACCTGTCT 35
```

Score = 20.3 bits (10), Expect = 244
Identities = 10/10 (100%), Gaps = 0/10 (0%)
Strand=Plus/Minus

```
Query 1225 TCTGCTATCA 1234
          |||||
Sbjct 37 TCTGCTATCA 28
```

Score = 18.3 bits (9), Expect = 965
Identities = 9/9 (100%), Gaps = 0/9 (0%)
Strand=Plus/Minus

```
Query 647 AATCTGACA 655
          |||||
Sbjct 28 AATCTGACA 20
```

> [gi|88687633|dbj|AB251241.1|](#) Mus musculus RNA for germline small RNA gsRNA271, complete
Length=26

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

```
Query 924 CAAGGCTGCCAC 935
          |||||
Sbjct 2 CAAGGCTGCCAC 13
```

> [gi|71612503|dbj|AB213806.1|](#) Synthetic construct DNA, reverse primer for microsatellite

Length=23

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

Query 111 AGCAAATATTAA 122
 |||||
Sbjct 19 AGCAAATATTAA 8

> [gi|71615529|dbj|AB213945.1](#) Synthetic construct DNA, forward primer for microsatellite
Length=22

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query 929 CTGCCACACTTT 940
 |||||
Sbjct 4 CTGCCACACTTT 15

> [gi|1340050|emb|Z73089.1|HSBTIII60](#) H.sapiens mRNA for T cell receptor beta chain V-D-J region (BV12BJ1S1; cell line BTIII 60)
Length=45

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query 173 AGACCACTGAAG 184
 |||||
Sbjct 23 AGACCACTGAAG 34

> [gi|9963961|gb|AF246208.1|F246197S12](#) Rattus norvegicus mitochondrial transcription factor VI - exon VII boundary; nuclear gene for mitochondrial product
Length=50

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query 66 TGCTAAAGATGA 77
 |||||
Sbjct 38 TGCTAAAGATGA 49

> [gi|1675337|gb|U71397.1|MMTFAM14](#) **G** Mus musculus mitochondrial transcription factor A (nuclear gene encoding mitochondrial protein, intron 6 and exon 7)
Length=50

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query 66 TGCTAAAGATGA 77

```
|||||||
Sbjct 35 TGCTAAAGATGA 46
```

> [gi|1675329|gb|U71386.1|MMTFAM06](#) **G** Mus musculus mitochondrial transcription factor A (nuclear gene encoding mitochondrial protein, exon 3 and intron 3)
Length=50

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

```
Query 1040 CTGCTTCTGGTA 1051
          |||||
Sbjct 32 CTGCTTCTGGTA 21
```

> [gi|425562|gb|S65766.1|S65766S1](#) COL4A5=type IV collagen alpha 5 chain [human, Alport syndrome Genomic Mutant, 34 nt, segment 1 of 2]
Length=34

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

```
Query 152 ATGATGGTATTT 163
          |||||
Sbjct 17 ATGATGGTATTT 28
```

Score = 18.3 bits (9), Expect = 965
Identities = 9/9 (100%), Gaps = 0/9 (0%)
Strand=Plus/Plus

```
Query 628 GATGGTTCA 636
          |||||
Sbjct 9 GATGGTTCA 17
```

> [gi|14277086|gb|AF357491.1|AF357491](#) Mus musculus clone MBI-72 miscellaneous RNA, partial
Length=48

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

```
Query 641 CAACTAAATCTG 652
          |||||
Sbjct 36 CAACTAAATCTG 47
```

> [gi|66353939|gb|AY227177.2|](#) Corvus monedula opsin (SWS1) gene, partial cds
Length=50

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

```
Query 1108 GAAGATGCAGCA 1119
          |||||
Sbjct 19 GAAGATGCAGCA 8
```

> [gi|38423190|emb|AJ538790.1|NTA538790](#) Nicotiana tabacum cDNA-AFLP-fragment BT1-M24-058
Length=34

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

```
Query 1282 ATCGAAGATGCT 1293
          |||||
Sbjct 13 ATCGAAGATGCT 2
```

> [gi|2564273|emb|AJ002273.1|MMAJ2273](#) Drosophila melanogaster troponin T gene, intron 3,
Length=43

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

```
Query 1334 TCCTGCAACAAG 1345
          |||||
Sbjct 42 TCCTGCAACAAG 31
```

> [gi|154705|gb|J01816.1|TIP58CG4](#) Integrated Ti plasmid (from A.tumefaciens), nopaline st
clone cg4, left end of T-DNA at host DNA/T-DNA border
Length=48

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

```
Query 898 CTTTATACGACA 909
          |||||
Sbjct 12 CTTTATACGACA 1
```

> [gi|51947981|gb|AY733733.1|](#) Macaca mulatta isolate 96e025-3q26.2 MLV-derived vector pro
integration site
Length=50

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

```
Query 1133 CTACCACCAACC 1144
          |||||
Sbjct 15 CTACCACCAACC 26
```

> [gi|15129391|dbj|AB068587.1|](#) Synthetic construct DNA, reverse primer for human STS sts-
at 1p36
Length=20

Score = 24.3 bits (12), Expect = 16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 714 AGCACAGAATGA 725
 |||||
 Sbjct 7 AGCACAGAATGA 18

> gi|15129302|dbj|AB068498.1 Synthetic construct DNA, forward primer for human STS sts-
 at 1p36
 Length=19

Score = 24.3 bits (12), Expect = 16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 845 ACAAAAAAGCTT 856
 |||||
 Sbjct 6 ACAAAAAAGCTT 17

> gi|15128874|dbj|AB068070.1 Synthetic construct DNA, forward primer for human STS sts-
 at 1p36
 Length=24

Score = 24.3 bits (12), Expect = 16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 485 AAGCAACTGGCA 496
 |||||
 Sbjct 4 AAGCAACTGGCA 15

> gi|216228|dbj|D13786.1|BACAAMSP Bacillus subtilis gene for alpha-amylase, partial cds,
 signal peptide
 Length=27

Score = 24.3 bits (12), Expect = 16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query 687 AGCACTCGCAGC 698
 |||||
 Sbjct 27 AGCACTCGCAGC 16

> gi|14586472|emb|AJ404691.1|MMU404691 Mus musculus partial mRNA for T-cell receptor al
 A4.1.E9
 Length=48

Score = 24.3 bits (12), Expect = 16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query 630 TGGTTCAGTAC 641
 |||||

Sbjct 18 TGGTTCAC TGAC 7

Score = 24.3 bits (12), Expect = 16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query 630 TGGTTCAC TGAC 641
 |||||
 Sbjct 18 TGGTTCAC TGAC 7

> [gi|913873|gb|S76024.1|S76024](#) {elementary chromomere pChM8} [mice, interphase chromosor
 Genomic, 47 nt]
 Length=47

Score = 24.3 bits (12), Expect = 16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 505 ATTTCTAAATTT 516
 |||||
 Sbjct 4 ATTTCTAAATTT 15

> [gi|56966056|pdb|1T9J|D](#) Chain D, I-Crei(Q47e)DNA COMPLEX
 Length=24

Score = 24.3 bits (12), Expect = 16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query 869 GTGAGACAGTTT 880
 |||||
 Sbjct 14 GTGAGACAGTTT 3

> [gi|56966055|pdb|1T9J|C](#) Chain C, I-Crei(Q47e)DNA COMPLEX
 Length=24

Score = 24.3 bits (12), Expect = 16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 869 GTGAGACAGTTT 880
 |||||
 Sbjct 11 GTGAGACAGTTT 22

> [gi|56966052|pdb|1T9I|D](#) Chain D, I-Crei(D20n)DNA COMPLEX
 Length=24

Score = 24.3 bits (12), Expect = 16
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Minus

Query 869 GTGAGACAGTTT 880
 |||||
 Sbjct 14 GTGAGACAGTTT 3

> [gi|56966051|pdb|1T9I|C](#) Chain C, I-Crei (D20n) DNA COMPLEX
Length=24

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query 869 GTGAGACAGTTT 880
 |||||
Sbjct 11 GTGAGACAGTTT 22

> [gi|55670022|pdb|1TRJ|B](#) Chain B, Homology Model Of Yeast Rack1 Protein Fitted Into 11.0
Cryo-Em Map Of Yeast 80s Ribosome
Length=41

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

Query 240 GGCAACTAACGG 251
 |||||
Sbjct 15 GGCAACTAACGG 4

Score = 18.3 bits (9), Expect = 965
Identities = 9/9 (100%), Gaps = 0/9 (0%)
Strand=Plus/Plus

Query 980 CGTTAGTTG 988
 |||||
Sbjct 5 CGTTAGTTG 13

> [gi|927128|gb|L36734.1|MUSIGDJAL](#) Mus musculus rearranged immunoglobulin heavy chain D-
(clone 20JH3)
Length=31

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

Query 1271 CCCGTAGCCGTA 1282
 |||||
Sbjct 20 CCCGTAGCCGTA 9

> [gi|13786782|pdb|1G9Z|E](#) Chain E, Laglidadg Homing Endonuclease I-Crei DNA PRODUCT COME
With Magnesium
Length=14

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

Query 869 GTGAGACAGTTT 880
 |||||

Sbjct 14 GTGAGACAGTTT 3

> [gi|13786777|pdb|1G9Y|D](#) Chain D, Homing Endonuclease I-Crei DNA SUBSTRATE COMPLEX WITH Calcium
Length=24

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query 869 GTGAGACAGTTT 880
 |||||
Sbjct 11 GTGAGACAGTTT 22

> [gi|13786776|pdb|1G9Y|C](#) Chain C, Homing Endonuclease I-Crei DNA SUBSTRATE COMPLEX WITH Calcium
Length=24

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

Query 869 GTGAGACAGTTT 880
 |||||
Sbjct 14 GTGAGACAGTTT 3

> [gi|180740|gb|M68994.1|HUM13COL25](#) Human alpha-1 type XIII collagen (COL13A1) gene, exon
Length=44

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query 806 TTGATGGTAAGT 817
 |||||
Sbjct 29 TTGATGGTAAGT 40

Score = 20.3 bits (10), Expect = 244
Identities = 10/10 (100%), Gaps = 0/10 (0%)
Strand=Plus/Plus

Query 891 CGCTGGCCTT 900
 |||||
Sbjct 21 CGCTGGCCTT 30

> [gi|4139431|pdb|1BP7|4](#) Chain 4, Group I Mobile Intron Endonuclease I-Crei Complexed With Homing Site Dna
Length=24

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

Query 869 GTGAGACAGTTT 880

```

          |||||
Sbjct  14  GTGAGACAGTTT  3

```

> [gi|4139430|pdb|1BP7|3](#) Chain 3, Group I Mobile Intron Endonuclease I-Crei Complexed With Homing Site Dna
Length=24

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

```

Query  869  GTGAGACAGTTT  880
          |||||
Sbjct  11  GTGAGACAGTTT  22

```

> [gi|4139429|pdb|1BP7|2](#) Chain 2, Group I Mobile Intron Endonuclease I-Crei Complexed With Homing Site Dna
Length=24

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

```

Query  869  GTGAGACAGTTT  880
          |||||
Sbjct  14  GTGAGACAGTTT  3

```

> [gi|4139428|pdb|1BP7|1](#) Chain 1, Group I Mobile Intron Endonuclease I-Crei Complexed With Homing Site Dna
Length=24

Score = 24.3 bits (12), Expect = 16
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

```

Query  869  GTGAGACAGTTT  880
          |||||
Sbjct  11  GTGAGACAGTTT  22

```

> [gi|88687684|dbj|AB251292.1|](#) Mus musculus RNA for germline small RNA gsRNA322, complete
Length=25

Score = 22.3 bits (11), Expect = 62
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

```

Query  780  TGGGAATGGTG  790
          |||||
Sbjct  11  TGGGAATGGTG  21

```

> [gi|88687467|dbj|AB251075.1|](#) Mus musculus RNA for germline small RNA gsRNA105, complete
Length=26

Score = 22.3 bits (11), Expect = 62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 972 AGGAAGCACGT 982
 |||||
 Sbjct 2 AGGAAGCACGT 12

> [gi|624799|dbj|D44509.1|BOVDIK08](#) Bos taurus DNA, microsatellite DIK016 PCR antisense pr
 Length=20

Score = 22.3 bits (11), Expect = 62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 712 AAAGCACAGAA 722
 |||||
 Sbjct 4 AAAGCACAGAA 14

> [gi|60099378|dbj|AB117772.1|](#) Arabidopsis thaliana AT3G27920.1 gene rearrangement juncti
 sequence, junction site 1, allele: gl1-3
 Length=47

Score = 22.3 bits (11), Expect = 62
 Identities = 14/15 (93%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query 395 CTAATGATGGTGAAA 409
 |||||
 Sbjct 19 CTAATGATAGTGAAA 33

> [gi|10242157|gb|AF254841.1|AF254841](#) Pyrococcus abyssi box C/D small nucleolar RNA sR8
 Length=50

Score = 22.3 bits (11), Expect = 62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Minus

Query 469 ATCGATGGCGC 479
 |||||
 Sbjct 19 ATCGATGGCGC 9

> [gi|10242139|gb|AF254823.1|AF254823](#) Pyrococcus abyssi box C/D small nucleolar RNA sR1
 Length=50

Score = 22.3 bits (11), Expect = 62
 Identities = 11/11 (100%), Gaps = 0/11 (0%)
 Strand=Plus/Plus

Query 581 GAGCTGTTAAA 591
 |||||
 Sbjct 11 GAGCTGTTAAA 21

> gi|438167|emb|Z22831.1|MMTCRVJAC M.musculus T cell receptor V alpha 8 F3.4 and T cell J alpha TA39 mRNA
Length=39

Score = 22.3 bits (11), Expect = 62
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Minus

Query 712 AAAGCACAGAA 722
 |||||||
Sbjct 14 AAAGCACAGAA 4

> gi|2288937|emb|AJ000950.1|SSAJ950 Sus scrofa EST 3'UTR CAP2A2 reverse primer
Length=22

Score = 22.3 bits (11), Expect = 62
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 377 TGAAAATTCAG 387
 |||||||
Sbjct 12 TGAAAATTCAG 22

> gi|1107766|emb|Z49031.1|MMTCR1242 M.musculus partial gene for T cell receptor gamma-cl CR124, _2)
Length=18

Score = 22.3 bits (11), Expect = 62
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Minus

Query 791 TATATTCTGCA 801
 |||||||
Sbjct 13 TATATTCTGCA 3

> gi|5804969|emb|AJ232730.1|MMU232730 Mus musculus mRNA for T cell receptor, clone T4.1.
Length=45

Score = 22.3 bits (11), Expect = 62
Identities = 11/11 (100%), Gaps = 0/11 (0%)
Strand=Plus/Plus

Query 78 CGCAGCAGGTC 88
 |||||||
Sbjct 3 CGCAGCAGGTC 13

gi|40791077|gb|CA585955.1| LBA00522.BOST4 cDNA from mouse aorta Mus musculus cDNA, mRNA sequence.
Length=36

Score = 32.2 bits (16), Expect = 0.24
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 796 TCTGCAGAAATTGATG 811
 |||||
Sbjct 20 TCTGCAGAAATTGATG 35

> ☐ gi|1321007|gb|W39290.1| zc76g04.r1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:3285' similar to WP:R13A5.13 CE01374 ;, mRNA sequence.
Length=49

Score = 30.2 bits (15), Expect = 0.95
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 966 GAAAAACAGGAAGCAC 980
 |||||
Sbjct 33 GAAAAACAGGAAGCAC 19

> ☐ gi|458592|gb|T17570.1| mps v30 The blue guys library Saccharomyces cerevisiae cDNA sec upstream of LacZ fusion similar to RNA12, S92205, mRNA sequence.
Length=43

Score = 30.2 bits (15), Expect = 0.95
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 360 TGCTGAAAATAATGA 374
 |||||
Sbjct 17 TGCTGAAAATAATGA 3

> ☐ gi|86584026|gb|DY248386.1| CSTCP1D0047A_655_691 CST-QuHSC Mus musculus cDNA, mRNA seq
Length=36

Score = 28.2 bits (14), Expect = 3.8
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus

Query 799 GCAGAAATTGATGG 812
 |||||
Sbjct 20 GCAGAAATTGATGG 7

Score = 20.3 bits (10), Expect = 916
Identities = 13/14 (92%), Gaps = 0/14 (0%)
Strand=Plus/Minus

Query 426 GGCAAAAATTGATG 439
 |||||
Sbjct 21 GGCAGAAATTGATG 8

> gi|598647|dbj|D17167.1| D17167 Kiseru Homo sapiens cDNA clone hmd2e06m3, mRNA sequence
Length=48

Score = 28.2 bits (14), Expect = 3.8
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

```
Query  873  GACAGTTTACAAAA  886
          |||||
Sbjct  22   GACAGTTTACAAAA  35
```

Score = 20.3 bits (10), Expect = 916
Identities = 13/14 (92%), Gaps = 0/14 (0%)
Strand=Plus/Minus

```
Query  359  TTGCTGAAAATAAT  372
          |||||
Sbjct  48   TTGCAGAAAATAAT  35
```

> gi|16838007|dbj|AV852668.1| AV852668 Nori Satoh unpublished cDNA library, egg Ciona ir
cDNA clone rcieg23b22 3', mRNA sequence.
Length=39

Score = 28.2 bits (14), Expect = 3.8
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

```
Query  396  TAATGATGGTGAAA  409
          |||||
Sbjct  25   TAATGATGGTGAAA  38
```

> gi|13554728|dbj|AU105207.1| AU105207 Sugano Homo sapiens cDNA library Homo sapiens cDN
KAT01893 5', mRNA sequence.
Length=50

Score = 28.2 bits (14), Expect = 3.8
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

```
Query  19   CTGAGCTCCGCCAT  32
          |||||
Sbjct  7    CTGAGCTCCGCCAT  20
```

> gi|13554727|dbj|AU105206.1| AU105206 Sugano Homo sapiens cDNA library Homo sapiens cDN
HRC08436 5', mRNA sequence.
Length=50

Score = 28.2 bits (14), Expect = 3.8
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

```
Query  19   CTGAGCTCCGCCAT  32
          |||||
```


Sbjct 12 CTGAGCTCCGCCAT 25

> [gi|13554726|dbj|AU105205.1](#) AU105205 Sugano Homo sapiens cDNA library Homo sapiens cDNA
HRC07843 5', mRNA sequence.
Length=50

Score = 28.2 bits (14), Expect = 3.8
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

Query 19 CTGAGCTCCGCCAT 32
 |||||
Sbjct 6 CTGAGCTCCGCCAT 19

> [gi|13554725|dbj|AU105204.1](#) AU105204 Sugano Homo sapiens cDNA library Homo sapiens cDNA
HRC06024 5', mRNA sequence.
Length=50

Score = 28.2 bits (14), Expect = 3.8
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

Query 19 CTGAGCTCCGCCAT 32
 |||||
Sbjct 5 CTGAGCTCCGCCAT 18

> [gi|13554720|dbj|AU105199.1](#) AU105199 Sugano Homo sapiens cDNA library Homo sapiens cDNA
HRC00642 5', mRNA sequence.
Length=50

Score = 28.2 bits (14), Expect = 3.8
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

Query 19 CTGAGCTCCGCCAT 32
 |||||
Sbjct 6 CTGAGCTCCGCCAT 19

> [gi|86580324|gb|DY244680.1](#) CSTBQ1D0647A_0_36 CST-BM Mus musculus cDNA, mRNA sequence.
Length=36

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

Query 383 TTCAGGTTGGTGC 395
 |||||
Sbjct 32 TTCAGGTTGGTGC 20

> [gi|82861917|gb|DR980846.1](#) SM016930 Placenta 3' EST Homo sapiens cDNA clone ID_16930 :
mRNA sequence.
Length=44

Score = 26.3 bits (13), Expect = 15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query 161 TTTCTGTTGCGCA 173
 |||||
 Sbjct 23 TTTCTGTTGCGCA 11

> [gi|82860386|gb|DR979315.1|](#) SM014071 Placenta 3' EST Homo sapiens cDNA clone ID_14071 :
 mRNA sequence.
 Length=48

Score = 26.3 bits (13), Expect = 15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query 370 AATGAAATGAAAA 382
 |||||
 Sbjct 30 AATGAAATGAAAA 42

Score = 24.3 bits (12), Expect = 59
 Identities = 15/16 (93%), Gaps = 0/16 (0%)
 Strand=Plus/Plus

Query 366 AAATAATGAAATGAAA 381
 |||||
 Sbjct 21 AAATGATGAAATGAAA 36

> [gi|67225679|dbj|BP915998.1|](#) BP915998 Adiantum capillus-veneris prothallium Adiantum ca
 cDNA clone YMU001_000081_F12, mRNA sequence.
 Length=46

Score = 26.3 bits (13), Expect = 15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query 349 GTGAAAGTCCTTG 361
 |||||
 Sbjct 9 GTGAAAGTCCTTG 21

> [gi|33679581|gb|CF307820.1|](#) ABF--01-G06.g1 ABF3-overexpressing transgenic rice plasmid
 library (ABF) Oryza sativa (japonica cultivar-group) cDNA
 clone ABF--01-G06, mRNA sequence.
 Length=39

Score = 26.3 bits (13), Expect = 15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

Query 1130 AATCTACCACCAA 1142
 |||||
 Sbjct 1 AATCTACCACCAA 13

> [gi|33679580|gb|CF307819.1|](#) ABF--01-G06.b1 ABF3-overexpressing transgenic rice plasmid

library (ABF) Oryza sativa (japonica cultivar-group) cDNA
clone ABF--01-G06, mRNA sequence.
Length=39

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query 1130 AATCTACCACCAA 1142
          |||||
Sbjct 39 AATCTACCACCAA 27
```

> ☐ [gi|33674726|gb|CF302965.1](#) 7LEAF--08-P09.b1 Rice leaf plasmid cDNA library II (7LEAF)
sativa (japonica cultivar-group) cDNA clone 7LEAF--08-P09,
mRNA sequence.
Length=47

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query 1130 AATCTACCACCAA 1142
          |||||
Sbjct 47 AATCTACCACCAA 35
```

> ☐ [gi|33672814|gb|CF301053.1](#) 7LEAF--05-M03.b1 Rice leaf plasmid cDNA library II (7LEAF)
sativa (japonica cultivar-group) cDNA clone 7LEAF--05-M03,
mRNA sequence.
Length=48

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query 1130 AATCTACCACCAA 1142
          |||||
Sbjct 48 AATCTACCACCAA 36
```

> ☐ [gi|33672140|gb|CF300379.1](#) 7LEAF--04-M01.b1 Rice leaf plasmid cDNA library II (7LEAF)
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-M01,
mRNA sequence.
Length=40

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query 1130 AATCTACCACCAA 1142
          |||||
Sbjct 40 AATCTACCACCAA 28
```

> ☐ [gi|33672066|gb|CF300305.1](#) 7LEAF--04-K12.b1 Rice leaf plasmid cDNA library II (7LEAF)
sativa (japonica cultivar-group) cDNA clone 7LEAF--04-K12,
mRNA sequence.
Length=48

Score = 26.3 bits (13), Expect = 15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query 1130 AATCTACCACCAA 1142
 |||||
 Sbjct 48 AATCTACCACCAA 36

> [gi|33670844|gb|CF299083.1|](#) 7LEAF--02-P01.b1 Rice leaf plasmid cDNA library II (7LEAF)
 sativa (japonica cultivar-group) cDNA clone 7LEAF--02-P01,
 mRNA sequence.
 Length=50

Score = 26.3 bits (13), Expect = 15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query 1130 AATCTACCACCAA 1142
 |||||
 Sbjct 50 AATCTACCACCAA 38

> [gi|33669672|gb|CF297911.1|](#) 7LEAF--01-B08.b1 Rice leaf plasmid cDNA library II (7LEAF)
 sativa (japonica cultivar-group) cDNA clone 7LEAF--01-B08,
 mRNA sequence.
 Length=39

Score = 26.3 bits (13), Expect = 15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus

Query 1130 AATCTACCACCAA 1142
 |||||
 Sbjct 39 AATCTACCACCAA 27

> [gi|26122450|gb|BQ592867.1|](#) E012123-024-028-N11-SP6 MPIZ-ADIS-024-developing root Beta
 cDNA clone 024-028-N11 5-PRIME, mRNA sequence.
 Length=43

Score = 26.3 bits (13), Expect = 15
 Identities = 19/21 (90%), Gaps = 0/21 (0%)
 Strand=Plus/Minus

Query 1165 GCATTGGCTAAAGTTGACAAT 1185
 |||||
 Sbjct 40 GCATTGGTTCAAGTTGACAAT 20

> [gi|20323261|dbj|AU258052.1|](#) AU258052 3'-directed mouse cDNA library Mus musculus cDNA
 BED0011943 3', mRNA sequence.
 Length=23

Score = 26.3 bits (13), Expect = 15
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Plus

```
Query 268 GATCTTTCTTCTA 280
          |||||
Sbjct 1 GATCTTTCTTCTA 13
```

> gi|13557556|dbj|AU108034.1 AU108034 Sugano Homo sapiens cDNA library Homo sapiens cDNA
COL07140 5', mRNA sequence.
Length=50

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

```
Query 694 GCAGCAGCGGCTA 706
          |||||
Sbjct 9 GCAGCAGCGGCTA 21
```

> gi|13555196|dbj|AU105675.1 AU105675 Sugano Homo sapiens cDNA library Homo sapiens cDNA
HEP03089 5', mRNA sequence.
Length=50

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query 967 AAAACAGGAAGCA 979
          |||||
Sbjct 24 AAAACAGGAAGCA 12
```

Score = 20.3 bits (10), Expect = 916
Identities = 10/10 (100%), Gaps = 0/10 (0%)
Strand=Plus/Plus

```
Query 1084 GGTGGTAGCC 1093
          |||||
Sbjct 29 GGTGGTAGCC 38
```

> gi|13552589|dbj|AU103068.1 AU103068 Sugano Homo sapiens cDNA library Homo sapiens cDNA
HSI02929 5', mRNA sequence.
Length=50

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query 79 GCAGCAGGTCAGG 91
          |||||
Sbjct 18 GCAGCAGGTCAGG 6
```

> gi|13552582|dbj|AU103061.1 AU103061 Sugano Homo sapiens cDNA library Homo sapiens cDNA
COLF1890 5', mRNA sequence.
Length=50

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)

Strand=Plus/Minus

```
Query  79  GCAGCAGGTCAGG  91
      |||
Sbjct  28  GCAGCAGGTCAGG  16
```

> [gi|6071458|gb|AW100845.1](#) sd62b05.y1 Gm-c1008 Glycine max cDNA clone GENOME SYSTEMS CI
ID: Gm-c1008-874 5', mRNA sequence.
Length=49

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query  804  AATTGATGGTAAG  816
      |||
Sbjct  28  AATTGATGGTAAG  16
```

> [gi|5425084|gb|AI813869.1](#) wk61b07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:24198
3' similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST ;contains
MSR1.b2 MSR1 repetitive element ;, mRNA sequence.
Length=40

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

```
Query  653  ACACAAACATAGC  665
      |||
Sbjct  1  ACACAAACATAGC  13
```

> [gi|3182248|gb|AA995759.1](#) os25e04.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:16063
3' similar to gb:V00567 BETA-2-MICROGLOBULIN PRECURSOR (HUMAN);,
mRNA sequence.
Length=35

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Minus

```
Query  1063  ATGTATCTGAGCA  1075
      |||
Sbjct  30  ATGTATCTGAGCA  18
```

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

```
Query  321  TGTATCTGAGCA  332
      |||
Sbjct  29  TGTATCTGAGCA  18
```

> [gi|2217095|gb|AA486931.1](#) ab17b11.r1 Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:841053 5' similar to gb:V00567 BETA-2-MICROGLOBULIN PRECURSOR

(HUMAN);, mRNA sequence.

Length=47

Score = 26.3 bits (13), Expect = 15
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus

Query 320 GTGTATCTGAGCA 332
 |||||
Sbjct 18 GTGTATCTGAGCA 30

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query 1064 TGTATCTGAGCA 1075
 |||||
Sbjct 19 TGTATCTGAGCA 30

> [gi|94359893|dbj|BY873732.1|](#) BY873732 Germination shoots Hordeum vulgare subsp. vulgare
clone bast73f12 3', mRNA sequence.
Length=43

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

Query 604 AATGATATTTTT 615
 |||||
Sbjct 15 AATGATATTTTT 4

> [gi|94351206|dbj|BY851751.1|](#) BY851751 Germination shoots Hordeum vulgare subsp. vulgare
clone bast43c08 5', mRNA sequence.
Length=34

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

Query 23 GCTCCGCCATTG 34
 |||||
Sbjct 33 GCTCCGCCATTG 22

> [gi|94344348|dbj|BY838005.1|](#) BY838005 Etiolated seedling shoot Hordeum vulgare subsp. v
cDNA clone baet133e11 5', mRNA sequence.
Length=34

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

Query 759 AACAACTGCAGC 770
 |||||
Sbjct 5 AACAACTGCAGC 16

```
> gi|93276160|gb|EB651462.1| GmUSCLM04pTriplEx216i23f1 Gillichthys liver & muscle libra
2 Gillichthys mirabilis cDNA clone 16i23 5', mRNA sequence.
Length=41

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus
```

```
Query 1135 ACCACCAACCCG 1146
          |||||
Sbjct 17 ACCACCAACCCG 28
```

```
> gi|90038657|emb|CT579987.1| CT579987 LG0ACA Pinus pinaster cDNA, mRNA sequence.
Length=50

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus
```

```
Query 42 CTCTTCTGGCCT 53
          |||||
Sbjct 25 CTCTTCTGGCCT 36
```

```
> gi|86584902|gb|DY249267.1| CSTFB1E0092A_78_127 CST-ProHSC Mus musculus cDNA, mRNA sequ
Length=49

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus
```

```
Query 788 GTGTATATTCTG 799
          |||||
Sbjct 17 GTGTATATTCTG 6
```

```
> gi|86581169|gb|DY245525.1| CSTBQ1D1085A_697_744 CST-BM Mus musculus cDNA, mRNA sequenc
Length=47

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus
```

```
Query 4 AAATCTCAGTCT 15
          |||||
Sbjct 11 AAATCTCAGTCT 22
```

```
> gi|86580675|gb|DY245031.1| CSTBQ1D0814A_96_144 CST-BM Mus musculus cDNA, mRNA sequence
Length=48

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus
```

```
Query 71 AAGATGACGCAG 82
```



```

          |||||
Sbjct  45  AAGATGACGCAG  34

```

> [gi|86578949|gb|DY243305.1|](#) CSTBQ1D0006A_0_33 CST-BM Mus musculus cDNA, mRNA sequence.
Length=33

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

```

Query  114  AAATATTAAAGG  125
          |||||
Sbjct   2    AAATATTAAAGG  13

```

> [gi|82578105|gb|DV749761.1|](#) ID0AAH2BH05ZM1 ID0AAH Acyrthosiphon pisum cDNA clone ID0AAH
5', mRNA sequence.
Length=38

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

```

Query  396  TAATGATGGTGA  407
          |||||
Sbjct  20   TAATGATGGTGA  9

```

> [gi|77991981|gb|DV467808.1|](#) est_t_truncatus843 HML_TuTr_IL-2 Tursiops truncatus cDNA, mRNA
sequence.
Length=18

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus

```

Query  1044  TTCTGGTAACAA  1055
          |||||
Sbjct  15    TTCTGGTAACAA  4

```

> [gi|77597704|gb|DV228503.1|](#) EST-AR183A10 Infected Porcine Peripheral Blood Cell cDNA 1:
Sus scrofa cDNA clone AR183A10, mRNA sequence.
Length=48

Score = 24.3 bits (12), Expect = 59
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus

```

Query  358  CTTGCTGAAAAT  369
          |||||
Sbjct  30   CTTGCTGAAAAT  41

```

> [gi|77498900|gb|DV212698.1|](#) 0089P0174Z_H04_T7 Mimulus guttatus library 2 Mimulus guttatus
cDNA clone 0089P0174Z_H04 5', mRNA sequence.
Length=34

Score = 24.3 bits (12), Expect = 59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 370 AATGAAATGAAA 381
 |||||
 Sbjct 17 AATGAAATGAAA 28

Score = 20.3 bits (10), Expect = 916
 Identities = 10/10 (100%), Gaps = 0/10 (0%)
 Strand=Plus/Plus

Query 191 TGAATGAAAT 200
 |||||
 Sbjct 15 TGAATGAAAT 24

> [gi|75475804|emb|AM075317.1|](#) AM075317 Chicken immune 2 - CSEQBN29 Gallus gallus cDNA c
 C0000466A11_T7, mRNA sequence.
 Length=20

Score = 24.3 bits (12), Expect = 59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 621 TGCAGCAGATGG 632
 |||||
 Sbjct 1 TGCAGCAGATGG 12

> [gi|86027041|gb|DR322794.1|](#) 143010 CERES-148 Arabidopsis thaliana cDNA clone 111205 5',
 sequence.
 Length=50

Score = 24.3 bits (12), Expect = 59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 960 AGCTAAGAAAAC 971
 |||||
 Sbjct 20 AGCTAAGAAAAC 31

> [gi|85905326|gb|DR226284.1|](#) 5735955 CERES-AL46 Arabidopsis thaliana cDNA clone 1143515
 mRNA sequence.
 Length=50

Score = 24.3 bits (12), Expect = 59
 Identities = 12/12 (100%), Gaps = 0/12 (0%)
 Strand=Plus/Plus

Query 37 CGTCTCTCTTCT 48
 |||||
 Sbjct 16 CGTCTCTCTTCT 27

> [gi|67567668|gb|DR108313.1|](#) JHU161B11L41 Canine cardiovascular system biased cDNA Canis

cDNA, mRNA sequence.

Length=41

Score = 24.3 bits (12), Expect = 59

Identities = 12/12 (100%), Gaps = 0/12 (0%)

Strand=Plus/Plus

Query	607	GATATTTTGT	618
Sbjct	5	GATATTTTGT	16

> gi|75922290|gb|AR703977.1| Sequence 7 from patent US 6929909
Length=18

Score = 32.2 bits (16), Expect = 2.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

```
Query  796  TCTGCAGAAATTGATG  811
          |||||
Sbjct  17   TCTGCAGAAATTGATG  2
```

> gi|42687870|gb|AR454420.1| Sequence 5 from patent US 6682741
Length=24

Score = 32.2 bits (16), Expect = 2.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

```
Query  354  AGTCCTTGCTGAAAAT  369
          |||||
Sbjct  16   AGTCCTTGCTGAAAAT  1
```

> gi|33751074|gb|AR350119.1| Sequence 58 from patent US 6586229
Length=24

Score = 32.2 bits (16), Expect = 2.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

```
Query  977  GCACGTTAGTTGTTAA  992
          |||||
Sbjct  23   GCACGTTAGTTGTTAA  8
```

> gi|92250878|dbj|BD359459.1| Process for the production of UDP-glucronic acid
Length=30

Score = 32.2 bits (16), Expect = 2.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

```
Query  545  TTGGCGGTGATGCTTA  560
          |||||
Sbjct  26   TTGGCGGTGATGCTTA  11
```

> gi|92244643|dbj|BD342484.1| Novel ubiquitin specific proteases
Length=33

Score = 32.2 bits (16), Expect = 2.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

```
Query  1236  CAACCTTGGCAACACC  1251
          |||||
Sbjct  33   CAACCTTGGCAACACC  18
```

> gi|92244642|dbj|BD342483.1 Novel ubiquitin specific proteases
Length=33

Score = 32.2 bits (16), Expect = 2.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus

Query 1236 CAACCTTGGCAACACC 1251
 |||||
Sbjct 1 CAACCTTGGCAACACC 16

> gi|21901300|emb|AX468464.1 Sequence 7 from Patent WO0222834
Length=18

Score = 32.2 bits (16), Expect = 2.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 796 TCTGCAGAAATTGATG 811
 |||||
Sbjct 17 TCTGCAGAAATTGATG 2

> gi|27949121|emb|AX590489.1 Sequence 1 from Patent WO02085933
Length=36

Score = 32.2 bits (16), Expect = 2.9
Identities = 28/32 (87%), Gaps = 0/32 (0%)
Strand=Plus/Plus

Query 1201 GGTGCAGTACAAAACCGTTTCGACTCTGCTAT 1232
 ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1 GGTGCGGTACAGAACCGTTTCAACTCCGCTAT 32

> gi|18093617|emb|AX322597.1 Sequence 58 from Patent WO0192539
Length=24

Score = 32.2 bits (16), Expect = 2.9
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus

Query 977 GCACGTTAGTTGTTAA 992
 |||||
Sbjct 23 GCACGTTAGTTGTTAA 8

> gi|18622154|dbj|E50954.1 Process for preparing Escherichia coli H antigen
Length=20

Score = 32.2 bits (16), Expect = 2.9
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 118 ATTAAAGGTCTGACTCAGGC 137

```

      ||||| |||||
Sbjct 1  ATTAAAGGCCTGACTCAGGC 20

```

> gi|56657472|gb|AR605808.1| Sequence 615 from patent US 6818751
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

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Query 451  GGCCTGGACGGTTTT 465
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Sbjct 25   GGCCTGGACGGTTTT 39

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> gi|56657468|gb|AR605804.1| Sequence 611 from patent US 6818751
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

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Query 451  GGCCTGGACGGTTTT 465
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Sbjct 22   GGCCTGGACGGTTTT 8

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> gi|56635885|gb|AR588988.1| Sequence 615 from patent US 6800746
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

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Query 451  GGCCTGGACGGTTTT 465
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Sbjct 25   GGCCTGGACGGTTTT 39

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> gi|56635881|gb|AR588984.1| Sequence 611 from patent US 6800746
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

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Query 451  GGCCTGGACGGTTTT 465
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Sbjct 22   GGCCTGGACGGTTTT 8

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> gi|77365703|gb|AR717054.1| Sequence 615 from patent US 6943236
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct   25  GGCCTGGACGGTTTT  39
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> gi|77365699|gb|AR717050.1| Sequence 611 from patent US 6943236
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct   22  GGCCTGGACGGTTTT  8
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> gi|53979053|gb|AR564002.1| Sequence 615 from patent US 6759515
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct   25  GGCCTGGACGGTTTT  39
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> gi|53979049|gb|AR563998.1| Sequence 611 from patent US 6759515
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct   22  GGCCTGGACGGTTTT  8
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> gi|40154459|gb|AR405622.1| Sequence 615 from patent US 6630305
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct   25  GGCCTGGACGGTTTT  39
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> gi|40154455|gb|AR405618.1| Sequence 611 from patent US 6630305
Length=46

Score = 30.2 bits (15), Expect = 11

Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct   22  GGCCTGGACGGTTTT  8
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> gi|40143650|gb|AR400355.1| Sequence 615 from patent US 6620922
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct   25  GGCCTGGACGGTTTT  39
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> gi|40143642|gb|AR400351.1| Sequence 611 from patent US 6620922
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct   22  GGCCTGGACGGTTTT  8
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> gi|74474231|emb|CS159058.1| Sequence 17 from Patent WO2005080576
Length=25

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

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Query  743  GAGTTGAATTCACAA  757
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Sbjct   17  GAGTTGAATTCACAA  3
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> gi|23320295|gb|AR219325.1| Sequence 56 from patent US 6420157
Length=30

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct   14  GGCCTGGACGGTTTT  28
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> gi|61890282|emb|CS051099.1| Sequence 24 from Patent WO2005021740
Length=25

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 743 GAGTTGAATTCACAA 757
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Sbjct 17 GAGTTGAATTCACAA 3

> gi|92345575|dbj|BD398016.1| COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF
CANCER
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 451 GGCCTGGACGGTTTT 465
|||||
Sbjct 25 GGCCTGGACGGTTTT 39

> gi|92345571|dbj|BD398012.1| COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF
CANCER
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 451 GGCCTGGACGGTTTT 465
|||||
Sbjct 22 GGCCTGGACGGTTTT 8

> gi|92331562|dbj|BD397081.1| DNA Encoding a Novel Prost 07 Polypeptide
Length=30

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 451 GGCCTGGACGGTTTT 465
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Sbjct 16 GGCCTGGACGGTTTT 30

> gi|60730322|emb|CS029344.1| Sequence 17 from Patent EP1510585
Length=25

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 743 GAGTTGAATTCACAA 757
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Sbjct 17 GAGTTGAATTCACAA 3

> gi|60730290|emb|CS029312.1| Sequence 24 from Patent EP1510573
Length=25

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 743 GAGTTGAATTCACAA 757
 |||||
Sbjct 17 GAGTTGAATTCACAA 3

> gi|92320083|dbj|BD437481.1| PROSTASE PROTEIN VACCINE COMPRISING DERIVATISED THIOL RES:
AND METHODS FOR PRODUCING SAID ANTIGEN
Length=30

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 451 GGCCTGGACGGTTTT 465
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Sbjct 13 GGCCTGGACGGTTTT 27

> gi|92289859|dbj|BD444719.1| COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF
CANCER
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 451 GGCCTGGACGGTTTT 465
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Sbjct 25 GGCCTGGACGGTTTT 39

> gi|92289855|dbj|BD444715.1| COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF
CANCER
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 451 GGCCTGGACGGTTTT 465
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Sbjct 22 GGCCTGGACGGTTTT 8

> gi|29712869|gb|AR278623.1| Sequence 615 from patent US 6512094
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct  25   GGCCTGGACGGTTTT  39
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> gi|29712865|gb|AR278619.1| Sequence 611 from patent US 6512094
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct  22   GGCCTGGACGGTTTT  8
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> gi|67590289|gb|AR657147.1| Sequence 615 from patent US 6894146
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct  25   GGCCTGGACGGTTTT  39
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> gi|67590285|gb|AR657143.1| Sequence 611 from patent US 6894146
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct  22   GGCCTGGACGGTTTT  8
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> gi|44845533|emb|CQ754277.1| Sequence 15 from Patent WO2004001069
Length=20

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

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Query  621  TGCAGCAGATGGTTC  635
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Sbjct  1    TGCAGCAGATGGTTC  15
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> gi|10025691|gb|AR096679.1|AR096679 Sequence 17 from patent US 6008193
Length=37

Score = 30.2 bits (15), Expect = 11

Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 65 GTGCTAAAGATGACG 79
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Sbjct 6 GTGCTAAAGATGACG 20

> gi|41014894|emb|CQ008203.1| Sequence 6843 from Patent WO0147944
Length=50

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

Query 1304 CCGAAGTGTCTAACA 1318
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Sbjct 18 CCGAAGTGTCTAACA 4

> gi|39722415|emb|AX816969.1| Sequence 12 from Patent WO03068819
Length=47

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

Query 467 ATATCGATGGCGCGC 481
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Sbjct 22 ATATCGATGGCGCGC 36

> gi|21694924|emb|AX446025.1| Sequence 2480 from Patent WO0216649
Length=24

Score = 30.2 bits (15), Expect = 11
Identities = 18/19 (94%), Gaps = 0/19 (0%)
Strand=Plus/Minus

Query 535 AACTATGATGTTGGCGGTG 553
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Sbjct 22 AACTATGAGGTTGGCGGTG 4

> gi|22205164|emb|AX469891.1| Sequence 8 from Patent WO02053771
Length=22

Score = 30.2 bits (15), Expect = 11
Identities = 18/19 (94%), Gaps = 0/19 (0%)
Strand=Plus/Plus

Query 358 CTTGCTGAAAATAATGAAA 376
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Sbjct 3 CTTGCTGAAAAAATGAAA 21

> gi|33036418|dbj|BD226648.1| Use of antiprolactin agent for remedy of hypercytosis
Length=20

Score = 30.2 bits (15), Expect = 11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 753 CACAACAACAACTGC 767
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 Sbjct 20 CACAACAACAACTGC 6

> gi|33036413|dbj|BD226643.1| Use of antiprolactin agent for remedy of hypercytosis
 Length=20

Score = 30.2 bits (15), Expect = 11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Minus

Query 753 CACAACAACAACTGC 767
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 Sbjct 20 CACAACAACAACTGC 6

> gi|32949314|emb|AX781460.1| Sequence 12 from Patent EP1321477
 Length=47

Score = 30.2 bits (15), Expect = 11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query 467 ATATCGATGGCGCGC 481
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 Sbjct 22 ATATCGATGGCGCGC 36

> gi|15863084|emb|AX248461.1| Sequence 540 from Patent WO0166800
 Length=31

Score = 30.2 bits (15), Expect = 11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query 1109 AAGATGCAGCAAAAT 1123
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 Sbjct 1 AAGATGCAGCAAAAT 15

> gi|16516314|emb|AX267641.1| Sequence 615 from Patent WO0173032
 Length=46

Score = 30.2 bits (15), Expect = 11
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus

Query 451 GGCCTGGACGGTTTT 465
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 Sbjct 25 GGCCTGGACGGTTTT 39

> gi|16516310|emb|AX267637.1| Sequence 611 from Patent WO0173032
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus

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Query  451  GGCCTGGACGGTTTT  465
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Sbjct  22   GGCCTGGACGGTTTT  8
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> gi|15390812|emb|AX200985.1| Sequence 615 from Patent WO0151633
Length=46

Score = 30.2 bits (15), Expect = 11
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

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Query  451  GGCCTGGACGGTTTT  465
          |||||
Sbjct  25   GGCCTGGACGGTTTT  39
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